STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _/0/583,//0_
Source: _1 Fwp_
Date Processed by STIC: _6/27/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/583,110_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _✓_ Invalid Line Length
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length
Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _✓_ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 _____ Use of <220>
Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 _____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa
"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFWP

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272006\J583110.raw

```
     2 <110> APPLICANT: Suntory Limited et al.
W--> 3 <120> TITLE OF INVENTION: Proess for production of yellow flowers by control of
flavonoid
W--> 4       synthesis system
W--> 5 <130> FILE REFERENCE: P952
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/583,110
C--> 6 <141> CURRENT FILING DATE: 2006-06-15
W--> 6 <160> NUMBER OF SEQ ID: 70
```

see pp 1, 3-12

ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed

```
W--> 7 <210> SEQ ID NO: 1
     8 <211> LENGTH: 1422
     9 <212> TYPE: DNA
E--> 10 <213> ORGANISM: ← mandatory response needed
W--> 11 <220> FEATURE:
W--> 12 <221> NAME/KEY:
     13 <222> LOCATION:
     14 <223> OTHER INFORMATION: Nucleic acid in pSPB1725
W--> 15 <400> SEQUENCE: 1
     16 atg gga gaa gaa tac aag aaa aca cac aca ata gtc ttt cac act tca        48
     17 Met Gly Glu Glu Tyr Lys Lys Thr His Thr Ile Val Phe His Thr Ser
     18  1               5                  10                  15
     19 gaa gaa cac ctc aac tct tca ata gcc ctt gca aag ttc ata acc aaa        96
     20 Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys
     21           20                  25                  30
     22 cac cac tct tca atc tcc atc act atc atc agc act gcc ccc gcc gaa       144
     23 His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu
     24           35                  40                  45
     25 tct tct gaa gtg gcc aaa att att aat aat ccg tca ata act tac cgc       192
     26 Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg
     27        50                  55                  60
     28 ggc ctc acc gcg gta gcg ctc cct gaa aat ctc acc agt aac att aat       240
     29 Gly Leu Thr Ala Val Ala Leu Pro Glu Asn Leu Thr Ser Asn Ile Asn
     30  65                  70                  75                  80
     31 aaa aac ccc gtc gaa ctt ttc ttc gaa atc cct cgt cta caa aac gcc       288
     32 Lys Asn Pro Val Glu Leu Phe Phe Glu Ile Pro Arg Leu Gln Asn Ala
     33              85                  90                  95
     34 aac ctt cga gag gct tta cta gat att tcg cga aaa tcc gat atc aaa       336
     35 Asn Leu Arg Glu Ala Leu Leu Asp Ile Ser Arg Lys Ser Asp Ile Lys
     36              100                 105                 110
     37 gca tta atc atc gat ttc ttc tgc aat gcg gca ttt gaa gta tcc acc       384
     38 Ala Leu Ile Ile Asp Phe Phe Cys Asn Ala Ala Phe Glu Val Ser Thr
```

file://C:\CRF4\Outhold\VsrJ583110.htm   6/27/2006

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,110**   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
39          115                  120                  125
40 agc atg aac ata ccc act tac ttc gac gtc agt ggc ggc gct ttt ctc     432
41 Ser Met Asn Ile Pro Thr Tyr Phe Asp Val Ser Gly Gly Ala Phe Leu
42      130                  135                  140
43 ctc tgc acg ttt ctc cac cac ccg aca cta cac caa act gtt cgt gga     480
44 Leu Cys Thr Phe Leu His His Pro Thr Leu His Gln Thr Val Arg Gly
45 145                  150                  155                  160
46 gac att gcg gat ttg aac gat tct gtt gag atg ccc ggg ttc cca ttg     528
47 Asp Ile Ala Asp Leu Asn Asp Ser Val Glu Met Pro Gly Phe Pro Leu
48                  165                  170                  175
49 att cac tcc tct gat tta cca atg agt ttg ttt tat cgt aag act aat     576
50 Ile His Ser Ser Asp Leu Pro Met Ser Leu Phe Tyr Arg Lys Thr Asn
51                  180                  185                  190
52 gtt tac aaa cac ttt cta gac act tcc tta aac atg cgc aaa tcg agt     624
53 Val Tyr Lys His Phe Leu Asp Thr Ser Leu Asn Met Arg Lys Ser Ser
54          195                  200                  205
55 ggg ata ctc gtg aac acg ttt gtt gcg ctc gag ttt cga gct aag gaa     672
56 Gly Ile Leu Val Asn Thr Phe Val Ala Leu Glu Phe Arg Ala Lys Glu
57      210                  215                  220
58 gct ttg tcc aac ggt ttg tac ggt cca act ccg cct ctt tat tta ctt     720
59 Ala Leu Ser Asn Gly Leu Tyr Gly Pro Thr Pro Pro Leu Tyr Leu Leu
60 225                  230                  235                  240
61 tca cat aca att gcc gaa ccc cac gac act aaa gtg ttg gta aac caa     768
62 Ser His Thr Ile Ala Glu Pro His Asp Thr Lys Val Leu Val Asn Gln
63                  245                  250                  255
64 cac gaa tgc cta tca tgg ctt gat ttg cag cct agt aaa agc gtg att     816
65 His Glu Cys Leu Ser Trp Leu Asp Leu Gln Pro Ser Lys Ser Val Ile
66                  260                  265                  270
67 ttc ctt tgt ttc gga aga aga gga gcg ttc tca gca caa cag ttg aaa     864
68 Phe Leu Cys Phe Gly Arg Arg Gly Ala Phe Ser Ala Gln Gln Leu Lys´
69          275                  280                  285
70 gaa att gcg ata ggg ttg gag aag agt gga tgt cga ttt ctt tgg ttg     912
71 Glu Ile Ala Ile Gly Leu Glu Lys Ser Gly Cys Arg Phe Leu Trp Leu
72      290                  295                  300
73 gcc cgc att tca ccg gag atg gac tta aat gcg ctt ctg ccg gag ggt     960
74 Ala Arg Ile Ser Pro Glu Met Asp Leu Asn Ala Leu Leu Pro Glu Gly
75 305                  310                  315                  320
76 ttt cta tcg aga act aaa gga gta ggg ttt gtg aca aac aca tgg gtg    1008
77 Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val
78                  325                  330                  335
79 ccg caa aaa gag gtg ttg agt cat gat gca gtg ggg ggg ttt gtg act    1056
80 Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr
81      340                  345                  350
82 cat tgc ggg tgg agt tcg gtt ctt gaa gcg ctg tcg ttc ggt gtc ccg    1104
83 His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro
84      355                  360                  365
85 atg att ggt tgg ccg ttg tac gca gag cag agg atc aat agg gtg ttc    1152
86 Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe
87      370                  375                  380
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110 TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
 88 atg gtg gag gaa ata aag gtg gcg ctg cca ttg gat gag gaa gat gga      1200
 89 Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly
 90 385                 390             395                 400
 91 ttt gtg acg gcg atg gag ttg gag aag cgc gtc agg gag ttg atg gag      1248
 92 Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu
 93             405             410             415
 94 tcg gta aag ggg aaa gaa gtg aag cgc cgt gtg gcg gaa ttg aaa atc      1296
 95 Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile
 96             420             425             430
 97 tct aca aag gca gcc gtg agt aaa ggt gga tcg tcc ttg gct tct ttg      1344
 98 Ser Thr Lys Ala Ala Val Ser Lys Gly Gly Ser Ser Leu Ala Ser Leu
 99             435             440             445
100 gag aag ttc atc aac tcg gtc act cgt taaag tttcttactc aatatatggt      1396
101 Glu Lys Phe Ile Asn Ser Val Thr Arg
102     450                 455
103 acatcggttt aactaccaaa ttttat                                         1422
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 457
107 <212> TYPE: PRT
108 <213> ORGANISM:
109 <223> OTHER INFORMATION: Amino acid sequence of 4,2',4',6'-tetrahydroxychalcane 4'-O-
110         glycosyltransferase encoded in pSPB1725
111 <400> SEQUENCE: 2
112 Met Gly Glu Glu Tyr Lys Lys Thr His Thr Ile Val Phe His Thr Ser
113   1                 5                 10                  15
114 Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys
115             20              25                  30
116 His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu
117             35              40                  45
118 Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg
119     50                  55                  60
120 Gly Leu Thr Ala Val Ala Leu Pro Glu Asn Leu Thr Ser Asn Ile Asn
121 65                  70                  75                  80
122 Lys Asn Pro Val Glu Leu Phe Phe Glu Ile Pro Arg Leu Gln Asn Ala
123             85                  90                  95
124 Asn Leu Arg Glu Ala Leu Leu Asp Ile Ser Arg Lys Ser Asp Ile Lys
125             100             105                 110
126 Ala Leu Ile Ile Asp Phe Phe Cys Asn Ala Ala Phe Glu Val Ser Thr
127         115             120                 125
128 Ser Met Asn Ile Pro Thr Tyr Phe Asp Val Ser Gly Gly Ala Phe Leu
129     130             135                 140
130 Leu Cys Thr Phe Leu His His Pro Thr Leu His Gln Thr Val Arg Gly
131 145             150                 155                 160
132 Asp Ile Ala Asp Leu Asn Asp Ser Val Glu Met Pro Gly Phe Pro Leu
133             165                 170                 175
134 Ile His Ser Ser Asp Leu Pro Met Ser Leu Phe Tyr Arg Lys Thr Asn
135             180                 185                 190
136 Val Tyr Lys His Phe Leu Asp Thr Ser Leu Asn Met Arg Lys Ser Ser
137     195                 200                 205
```

(handwritten annotations in margin:) E--> ← mandatory response   insert this mandatory numeric identifier <220> wherever <221>, <222>, or <223> is shown

(handwritten mark near line 111) E -->

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
138 Gly Ile Leu Val Asn Thr Phe Val Ala Leu Glu Phe Arg Ala Lys Glu
139     210             215             220
140 Ala Leu Ser Asn Gly Leu Tyr Gly Pro Thr Pro Pro Leu Tyr Leu Leu
141 225             230             235             240
142 Ser His Thr Ile Ala Glu Pro His Asp Thr Lys Val Leu Val Asn Gln
143             245             250             255
144 His Glu Cys Leu Ser Trp Leu Asp Leu Gln Pro Ser Lys Ser Val Ile
145             260             265             270
146 Phe Leu Cys Phe Gly Arg Arg Gly Ala Phe Ser Ala Gln Gln Leu Lys
147         275             280             285
148 Glu Ile Ala Ile Gly Leu Glu Lys Ser Gly Cys Arg Phe Leu Trp Leu
149     290             295             300
150 Ala Arg Ile Ser Pro Glu Met Asp Leu Asn Ala Leu Leu Pro Glu Gly
151 305             310             315             320
152 Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val
153             325             330             335
154 Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr
155             340             345             350
156 His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro
157         355             360             365
158 Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe
159     370             375             380
160 Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly
161 385             390             395             400
162 Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu
163             405             410             415
164 Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile
165             420             425             430
166 Ser Thr Lys Ala Ala Val Ser Lys Gly Gly Ser Ser Leu Ala Ser Leu
167         435             440             445
168 Glu Lys Phe Ile Asn Ser Val Thr Arg
169     450             455
281 <210> SEQ ID NO: 13
282 <211> LENGTH: 1446
283 <212> TYPE: DNA
284 <213> ORGANISM:
285 <220> FEATURE:
286 <221> NAME/KEY:
287 <222> LOCATION:
288 <223> OTHER INFORMATION: pSPB264
289 <400> SEQUENCE: 13
290 atgggaaaac ttcacattgc cttatttcca gttatggctc atggtcacat gatcccaatg     60
291 ttggacatgg ccaagctctt tacctcaaga ggcatacaaa caacaatcat ttcgactctc    120
292 gccttcgctg atccgataaa caaagctcgt gattcgggcc tcgatattgg actaagcatc    180
293 ctcaaattcc caccagaagg atcaggaata ccagatcaca tggtgagcct tgatctagtt    240
294 actgaagatt ggctcccaaa gtttgttgag tcattagtct tattacaaga gccagttgag    300
295 aagcttatcg aagaactaaa gctcgactgt ctcgtttccg acatgttctt gccttggaca    360
296 gtcgattgtg cggctaagtt cggtattccg aggttggttt tccacggaac gagcaacttt    420
297 gcgttgtgtg cttcggagca aatgaagctt cacaagcctt ataagaatgt aacttctgat    480
```

E--> (handwritten note at line 284): ← *mandatory response*

(handwritten note at line 288): ← *if this explains an Artificial Sequence, give source of genetic material*

W--> marks at lines 285, 286, 289.

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
298 actgagacat ttgttatacc ggatttcccg catgagctga agtttgtgag gactcaagtg    540
299 gctccgtttc agcttgcgga aacggagaat ggattctcaa agttgatgaa acagatgacg    600
300 gagtctgttg gtagaagcta cggtgttgtg gttaacagtt tttatgagct cgagtcgact    660
301 tatgtggatt attacagaga ggttttgggt agaaagtctt ggaatatagg gcctctgttg    720
302 ttatccaaca atggcaatga ggaaaaagta caaggggaa aggaatctgc gattggcgaa    780
303 cacgaatgct tggcttggtt gaattccaag aagcagaatt cggttgttta cgtttgtttt    840
304 ggaagtatgg cgactttac tccagcgcag ttgcgcgaaa ctgcgattgg actcgaggaa    900
305 tcaggccaag agttcatttg ggtagttaaa aaggccaaaa acgaagaaga aggaaaagga    960
306 aaagaagaat ggctgccaga aaattttgag gaaagagtga aagatagagg cttgatcata   1020
307 agaggatggg cgccgcaatt gttgatactc gatcatcctg cggtaggagc tttcgtgacg   1080
308 cattgtggat ggaattcgac gttggaagga atatgcgccg gtgtgcctat ggtgacttgg   1140
309 ccagttttcg cagagcagtt tttcaatgag aagtttgtga cagaggtttt ggggaccggt   1200
310 gtttcggttg ggaataagaa gtggctaagg gcagcaagtg aaggtgtgtc gagggaggca   1260
311 gtgacgaacg cggtgcagcg tgttatggtg ggagaaaatg cgtcggagat gagaaagcga   1320
312 gcgaagtatt ataaggaaat ggcgaggcgg gcggttgagg aaggcggttc gtcttataat   1380
313 ggtttgaatg agatgataga ggatttgagt gtgtaccgtg ctccagaaaa acaagactta   1440
314 aactag                                                              1446
316 <210> SEQ ID NO: 14
317 <211> LENGTH: 1488
318 <212> TYPE: DNA
319 <213> ORGANISM:
320 <220> FEATURE:
321 <221> NAME/KEY:
322 <222> LOCATION:
323 <223> OTHER INFORMATION: pSPB662
324 <400> SEQUENCE: 14
325 atggcctttc aaattcaacc agagcttcta aacttcgttt tcataccatt catggcccct     60
326 ggccactcaa tccctatgat agacttagcc aaattattcg cggaacgcgg cgtcaacgta    120
327 acgatcatcg taacacctct taacgccgca cgattcaatt ccgttattaa tcgagccgtt    180
328 gaatcaggac agtccattcg tcttctccaa gtaaaattcc ctggtgaaga agccgggttg    240
329 ccacctggat gcgaaagcgc cgagacttta ccatcttatg aattgattcc aaattttttt    300
330 accgccgtaa aaatgttaca acaaccaatc gaggaagaat tgagaaattt gatccctttta   360
331 ccaagctgcg tcatttgtga taaacacata ccctggactg ctcaaacgtg caagaatctc    420
332 cgaattccga ggataatttt cgatggaatg agctgttttg ctcctttagt aacacacgtt    480
333 ctctacgtgt ctaaggttca tgaaaccgtt cctccaaacg agccgttcgt tgttcctgat    540
334 ttccccgatg agatagagtt aacgaggttt caattgccag ggttgttgaa tccaagtcca    600
335 aggataaatt tttacgattt tcgcgaacaa gtgaagaaaa ctgaggagga ggcttatggg    660
336 gtggtggtga acagttttga ggagctggaa aaagattatt cgagatgtt tcggaaattg    720
337 aaagggggta agtttggtg tgttgggcct ttgtcgcttt atggtaacga cgatttggac    780
338 agggctggaa gagggaataa ggcgtcgatt gatacggatc ggtgtatgaa atggcttgat    840
339 gatatgaaac cagaatctgt aatttatgcc tgtttgggaa gcctgagtcg tttgtcgcgt    900
340 tcacagttcg tcgaacttgc tttgggattg gaagcatcaa aacactcgtt tgttctagtt    960
341 gttaaaaccg aaggagagaa gtcgttggaa atagagaaat ggattttgga caatggattc   1020
342 gaggaaagaa cgaaagatag agggttcttg attcgtggtt ggtcgccaca agtgttgatc   1080
343 ttgtcgcatt ttgcagtggg aggattcttg acgcattgtg gttggaattc gacgcttgag   1140
344 ggcatttgtg ctggtttgcc aatggtgatg tggccgatgt cggcgaaca gtttttgaat   1200
345 gagaagttag tggtgcagat tttggggacg ggtgtgggag ttggagcgaa aagtacggta   1260
346 catttggggg atgaagagat ggatgagatg agagtgacga ggaaggggat taccaaggcg   1320
347 gtcgtggcag ttatggatag aggaactgaa gggtgtgaga ggcggagaaa ggcgaaggag   1380
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RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

          Input Set : A:\PTO.RJ.txt
          Output Set: N:\CRF4\06272006\J583110.raw

```
      348 cttggtgaaa tggctaagag ggcagtccaa gttgggggat cttcatgtaa gaatgtcgac   1440
      349 cagctaattc aagaagttgc accattgagt gtagcgaggg atgtgtaa                 1488
      351 <210> SEQ ID NO: 15
      352 <211> LENGTH: 1446
      353 <212> TYPE: DNA              response needed
E--> 354 <213> ORGANISM:
W--> 355 <220> FEATURE:
W--> 356 <221> NAME/KEY:
      357 <222> LOCATION:
      358 <223> OTHER INFORMATION: pSPB1621
W--> 359 <400> SEQUENCE: 15
      360 atgggttctc tccctgaaaa tgagctcaac aaaccacatg ctgtgtgcat accctatcca    60
      361 gcactagggc atttcagtcc catgctagat tttgctaagc tcctccacca aaaaggcttt    120
      362 cacataacct tcgtcaacac cgagtacatc cgtctccgcc tcctcaagtc ctgtggccct    180
      363 gccgccctgg acgggctacc ggactttcgc ttcatgacta tccccgatgg cctccctttg    240
      364 tcggacgacg tttcgcgtga tgtcgcttcc atttctgtct ctactaacaa aacttgctta    300
      365 gaaccctttt gtgaggtgct atcggacctc atggataatg gttccaaccc gccggtgagc    360
      366 tgcattgtgt ccgacggggt aatgagtttc acccttgagg cggcggagag gtttggactg    420
      367 ccagaggtgc tgttctggac gcccgctgct tgtggcatct tagctttcac gcagtataag    480
      368 catcttgtgg agagaggata tgtacctctc aaagatacga gccaggtaac aaatggctac    540
      369 ctggaaacaa tattagattg ggttccaggg atgaaggata ttcgattgag ggaattccca    600
      370 actttcataa gaacgacgga cccaaacgac gttatgctgg attttctaat aaaacaagtt    660
      371 gacgccaccc cgaaagccaa tgctgtgatc atcaacacgt tcgacacatt ggaaagtgac    720
      372 gctctcaacg ccctctctgt catgtttccg cgcatataca cactcgggcc tctccatatg    780
      373 atgttgaata atcccgaggt cgacgaaccc tctaatgcaa tcaaatttaa tctttggaaa    840
      374 gaagactcac attgcctaga ttggctcgat gtgaacgagc ccggatcagt tgtatacgtg    900
      375 aattttggca gctcaacaat tctgactgtt gaacaactaa ctgaattagc atggggcctt    960
      376 gctaacagca agaaaccgtt cctttggatc atcaggcctg atttagtaac tggtgcatcc   1020
      377 tccatgcttc cgcctgagtt cctggtcgag actaaagaca gaagcatgtt agtgagttgg   1080
      378 tgcaaccaag aacaagtgtt gaagcacccc gcgactggag tgttcttgac gcattgtgga   1140
      379 tggaattcga cgattgaaag catttgcagc ggcgtgccaa tgatttgttg gccttactac   1200
      380 gctgagcagc aaaccaactg taggtacagt tgtgtggaat gggaaatagg aatggagatc   1260
      381 attgacaacg atgtgaagag agatgaggtg gaattgctgg tgattaagtt gatggatggt   1320
      382 atcaagggaa agaaaatgaa aaagaaagct atggagtgga agaggaaagc agaagaggcg   1380
      383 gtagcttttg ggggctcttc ctacatgaat ttggataaac ttattagcga cgtgcttttt   1440
      384 ccataa                                                              1446
      386 <210> SEQ ID NO: 16
      387 <211> LENGTH: 1458
      388 <212> TYPE: DNA              response needed
E--> 389 <213> ORGANISM:
W--> 390 <220> FEATURE:
W--> 391 <221> NAME/KEY:
      392 <222> LOCATION:
      393 <223> OTHER INFORMATION: pSPB1620
W--> 394 <400> SEQUENCE: 16
      395 atggcaggtc caaattgcaa gcctcacgcc atcatgatcg cacttcctta ccaaggccac    60
      396 ataactcctt ttgtcaatct tgcactaaaa cttgcttcca atggctttac aatcactttt    120
      397 gttcaccttg aatttatcca ccaaatgttg tctaaagccc ataacgccac taaaactgaa    180
      398 gcagatttat tttcggaagc acgagaatcc ggtctcgaca tacgttacac aacgattgac    240
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
399 gatggtttcc ctttggaatt cgacagggct ctccactccg aggagtattg gcactccatg   300
400 ttgcgagatt tcccgttaca cgtcgatgag tttgttcgaa aagtcgtgga gtcagagcca   360
401 tttttagagc acttttttggt tacggatact atgtatacat ggcctgcaac cattgcaaag   420
402 aaacataatc ttgtgaatat ttcgttttgg actgaaccag ccctggtgtt ttctttgtct   480
403 taccatataa accttctgaa gcaaaatggt cattttccat gtaaagaaaa tattgatgag   540
404 gaaataaatt acgtaccagg agttgattca ataagtacaa gggatttaat gtcttatttt   600
405 aaagaaccag gatcagaaac attagagaaa aatgttgtgc tcaaggcatt tgaaggagtg   660
406 aagaaagctg atttcatctt gcataacaca ttgcaagaac tagaatctga gacactctca   720
407 gctcttacca aaatgcagcc aaattacgcc gttggaccta ttaatttctc caaacatact   780
408 cctaaaactg tcaccaagag tctacggtct gaattcgact gcaccaactg gctcgactct   840
409 aagcctccca actctatttt atacgtctcg tttggtagtt ttattcagac aagcaaagag   900
410 gtaattgaag aaatcgctta cggtcttctc cttagtgaag ttaactttat atgggtggtt   960
411 agaacagata gtgtgagttt agaggataac gaggttttgc cggttggatt tagggatgag  1020
412 gttaaagata gggggttgat agttccgtgg tgtgatcaaa ttacggtttt gtctaatcgc  1080
413 gcggttggag gattcttgac gcattgtgga tggaactcgg tattagagag tatgtggtgt  1140
414 ggcgttccta tgatttgtta tccgttaaca tatgatcaac ctactaatag gaaactattg  1200
415 gttgatgatt ggaagattgg cattaatctt tgcgacggag cgttgattaa tagaaaagaa  1260
416 attgcagaga agattaaggc cttgatgagt gaaagtactt cagagggtt gagggaagaa  1320
417 tctgagaaag ttaagggctt gttgaagaat gcactggaag ttggtggttc atcagagaag  1380
418 aatttcaata aatttattga ggatttgaag gcaaaaattc aaataatgaa agagcaaatg  1440
419 cctgctaata ccagttga                                                1458
421 <210> SEQ ID NO: 17
422 <211> LENGTH: 1443
423 <212> TYPE: DNA
```

E--> 424 <213> ORGANISM: *response needed*
W--> 425 <220> FEATURE:
W--> 426 <221> NAME/KEY:
```
427 <222> LOCATION:
428 <223> OTHER INFORMATION: pSPB1622
```
W--> 429 <400> SEQUENCE: 17
```
430 atgggttcca cagccgaaaa taaacagaaa acccacattg tgtgcatacc ctacccagcc    60
431 caggggcaca tcagccccat gctaaagtta gccaaactgc tacaccaaaa cggctttttac  120
432 atcactttttg tcaacacgga gtacaaccac cgccgcctca tcaagtcccg cggccccacc   180
433 gccctcgacg gattgcccga tttccggttc gttacgatcc ccgacgggct tcctttctct   240
434 gaagccgacg ccacacagga tatcccttct ctttgtgttt caaccaccaa cacttgcttg   300
435 gagcccttttt gcgagctgct gtcgaacctc aataactccg gcccggacgt gcccccggtg   360
436 agctgcatcg tatccgatgg tgtcatgagc ttcacgttga aggcggcgga gagatttggg   420
437 ctgccggagg tgctgttctg gacgacgagt gcgtgtgggt cttggcgta tacgcagtat   480
438 aagcatctcg tggagaaagg ctatgtaccc ctcaaagata tgagccaagt aacggatgga   540
439 tatttgaaaa caagcatgga ctggattcca ggaacgaagg acatccaact aagggacttc   600
440 ccctctttca tcaggacaac agatccagaa gacatcatgc ttaatttttt aatacaagaa   660
441 actgatgttg ttccgagagc caaagctgta ataatcaaca ccttcgacat gttagaacac   720
442 gacgtcctgg aagcgctctc caccatgttt tcacgcgttt acagcatcgg ccctcttcag   780
443 ctgatgatga attatgttca caacgagtcc cttaaatcca tcagttccag tctatggaaa   840
444 gaagaaacac attgcgtcga ttggctcgat tcaaaggagc ccgaatccgt tgtgtacgta   900
445 aattttggca gcataactgt cgtgactgca gaacaactga ctgagtttgc gtggggggctc   960
446 gctaatagta agaagacttt cctatgggtt attaggcctg atatagttgc tggagactcg  1020
447 gctatgctgc cccctgaatt cgtgacgggg acaaaagata gaagcatgtt aatcagctgg  1080
448 tgtaaccaag aacaggtgtt gaatcaccca tcaattggag ggttttttgac gcacagtggt  1140
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272006\J583110.raw

```
449 tggaattcga cgattgaaag tatagtcgag ggagttcctg tgatttgctg gcctttcttt    1200
450 gctgagcagc aaacaaattg taggttcagt tgcgtggaat gggaaatagg aatggagatt    1260
451 gataataatg tgaagagaga tgaggttgaa gttttggtga gggaattgat ggatggagag    1320
452 aggggaaga aaatgaagga gaaagctatg gagtggaaag ggaaagcatt agaggcaact     1380
453 gcacttgggg gctcttccta cttgaacttg gaaaaactaa ttaaggaggt gcttttgcat     1440
454 taa                                                                   1443
456 <210> SEQ ID NO: 18
457 <211> LENGTH: 1407
458 <212> TYPE: DNA
E--> 459 <213> ORGANISM:  ⟵response needed
W--> 460 <220> FEATURE:
W--> 461 <221> NAME/KEY:
462 <222> LOCATION:
463  <223> OTHER INFORMATION: pSPB1610
W--> 464 <400> SEQUENCE: 18
465 atggcatctt ctccccataa ccagccaacc acgccccgcc acgtggtggc cctaccctac      60
466 cccggccgcg gccacataaa ccccatgctc aacatctgca aagccgtagc ggagaagagc     120
467 agccacatca acataacaat catcctaacc gaggaatggc tcggcttaat cggctcagcc     180
468 gacaagccgc cgaacataag ctacgccgcg ataccgaaca ttctgccgtc ggagcacgtt     240
469 cgcggcgagg atccacatgg tttttgggcg ctgtttggc agaagatgga ggagccggtt      300
470 gatcggctgc tggacgagct tcggcttaat aataacaagc cggagtttgt gatagccgat     360
471 gctttcttgc attgggcggc tgacgtggcg ggcaggagga atattccctt ggcatctgtt     420
472 tggccaatgt cggcgtccac gttcacggtg ctttaccact ttgaccttct cgttgaccac     480
473 ggacactttc cgatcgacat accagtgaat ggagatgcta ttgtggatta catcccggga     540
474 ctccctccag ttcgcgtcgc agattttcca aaagacataa gaaaacaaga agacgcatcc     600
475 ttcgtcctta aactcattcc caactcacca aaattcatca tcttcacttc aatttacgac     660
476 ctcgaatcca agatcatcga cgctctaaag caaaaatctt ccttctcaat ctacaacatt     720
477 ggtcctcatg cttcctattc caaactcaaa cacatcctca actcggataa aatcacgaaa     780
478 cctgatcaag ataaccccga ctacttaaaa tggttagatc tccaacctcc caactccgtc     840
479 ttgtacattt cactcggcag tttcctatcc atttcgcag cccaaatgga tgaactcgca      900
480 accggaatac gaaactctgg tgtccgcttt ttgtgggtgg cacgtggcga aacaaaccgg     960
481 ttgaaagaga tttgttgtga tcatgaaaag gggctgatca tagaatggtg cgatcaaatg    1020
482 caggttcttt ctcattcttc ggttggtgga ttcttgtcgc attgtggttg gaattcgact    1080
483 aaagaggcgt tgatggccgg ggtgccgttt ttgactattc caattatgtt tgatcaagtg    1140
484 tctaacgcga aggcggtcgt ggaagattgg agggtggggt ggagggtggt gaatgagttt    1200
485 aatgaagaag agttggtggg aggagatgag attgcgaata ttgtgaggag gtttatggat    1260
486 atggaaaatg gtgagaggaa agagttgacg aaaaatgtga aagaggtgca gaagatttgt    1320
487 gcgagagagt tcgaagatgg agatggacag tcgtttgagt ttaatgttga agtttggtt    1380
488 caattgattc tgcaattggg tccgtaa                                        1407
490 <210> SEQ ID NO: 19
491 <211> LENGTH: 1428
492 <212> TYPE: DNA
E--> 493 <213> ORGANISM:  ⟵response needed
W--> 494 <220> FEATURE:
W--> 495 <221> NAME/KEY:
496 <222> LOCATION:
497 <223> OTHER INFORMATION: pSPB1609
W--> 498 <400> SEQUENCE: 19
499 atgaacaaca caacccaaca acaaacagta gcattagcac tagcacctca ctgtttaatc      60
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
500  gtcccattcc cattccaagg ccacattaac cccttactcc aattcgccaa acgcctcata    120
501  actcaccaca acaaaaacct ccaaatcaca ttcgcactca ccaaattcat cctcaccaac    180
502  ctctcctccg gtgccggaga atcatccttc tctctccggt caatctccga cggcttcgac    240
503  gccggcggcc gcgctcaggc caactccggc gccgaatacc tctccaaatt ccgcgagatc    300
504  ggatctcaaa ccctaaccga acttatccaa gacctatccg aatcgggtcg acccgttgac    360
505  tgcgtggtct acgacccgtt cgtaccttgg gccttagatg ttgccaaggg taaattcgga    420
506  atttcaacgg cggcgttttt tacgcagtcg tgtgcggtgg ataatatata cagtcgggtt    480
507  tataacggcg atttggagct gccgttgccg gagaatgagg tggttagggt tccgggtttg    540
508  ccggagatgg agccgtttga gatgccgagc tttgtgtatt taaacgggtc gtacccgtcg    600
509  agttttgaga tggttgtggg tcagtttagg aatgttgatg aggcggattg ggtttttgtc    660
510  aacacttttt atgagttgga gaaagaggtc attgactgga tgtcaaaatc ttggcgagtg    720
511  aaagcaattg gacctaccat accatcaatg ttcatggaca agagattgca agaggacaaa    780
512  tcatacggtc ttagcatgtt caagcataca acaaatgact gcataaattg gctcaacgga    840
513  aaacaatcaa aatccgtcat ttatgtcgca tttggaagtc ttgcagaatt atcccacgac    900
514  caaactcaag aactggcaca cgccttaaca acctacgaca aacacttctt atgggttgta    960
515  cgatcatcgg aagaagctaa gcttccccaa aattttgcta acgaaacatc taagaaaggg   1020
516  ttgatagtgt cgtggtgccc tcaattagag gtcttgtcgc acgaggccat cggttgtttc   1080
517  gtgactcatt gtggttggaa ttcaacgctc gagggattga gtttgggggt gcctatggtg   1140
518  gcgatgccac agtggacgga tcagagtacg aacgctaagt ttatcgtgga tgtttggggt   1200
519  gtgggtgttc gggctaaggt ggacgagggg ggattagcga ggcaagatga gatagttcgt   1260
520  tgcttaggga gcgtcatgga aggggagaac ggagaaaaga taagaaagaa tgcgaatgaa   1320
521  tggaaggaac gggcgtgcaa tgcagttgat gaaggggggga gttcagacaa aaatattgaa   1380
522  gaatttgtta ctacgttgat aagttcccat gacttgcgtc aagagtaa             1428
524  <210> SEQ ID NO: 20
525  <211> LENGTH: 1425
526  <212> TYPE: DNA
```

E--> 527 <213> ORGANISM: ← *response needed*
W--> 528 <220> FEATURE:
W--> 529 <221> NAME/KEY:
```
530  <222> LOCATION:
531  <223> OTHER INFORMATION: (pSPB1617)
```
see p. 10
W--> 532 <400> SEQUENCE: 20

```
533  atgtctagtg agagccaaat aaacttagtg ttcatccctc tccctgtaaa gggacacatt     60
534  gtctcaacgc tagagacggc aaagctactc gtcgatcgaa acaaacgcct caccatcaca    120
535  atcctcctca tgaagctgcc agtcgacgcc aaggtagatg attccttcac aaaaaatccc    180
536  tcctgctctc aaataacttt tgtacatctc cctcgaatcg agcacagttc catggaacca    240
537  ccgggaactc ccgaatcctt tgtacacagg ttcgtcgaga gccaaaaatg tctcgtaaga    300
538  gatgcggtgg ttaaagcaac ggagggctca aaatcaaaca ggctagccgg atttgtaatc    360
539  gacatgttct gcaccccgat gattgatgtg gccaatgaat ttggcgtccc gacatacgtg    420
540  gctttcacgt ccggggccgc aactctcggg ctattgttcc atttgcagag tcttagagat    480
541  gaatttaatc aggacgtgaa ggagtacgag aactcggaag ttgagatatc gatcccggct    540
542  tatgttaacc cgttcccttc caaatccttg ccgtctcctg tcttcaacga ggacggtgtt    600
543  tttcttagtc ttgcaaaggg gttcagagag gctaaggta tattgatcaa cacctttta     660
544  gaatttgaat cccatgccat taaatcgctc tccaacgatg cgagaatccc gcctgtttac    720
545  cccatcgggc cagtaattca cgccacggaa gataatgcaa acaaaggaaa gcaggacgaa    780
546  atcatcgcgt ggcttgacga gcaacctgat tcatccgtcg tgtttctttg cttcggaagc    840
547  gctggatgct ttgaagaaaa tcaagtgaag gagattgcag tggcgctcga caaaagtgga    900
548  taccggtttt tatggtcatt gagaaagccg cctcccaaag aaaaagcgga gtttccaggg    960
549  gagtacaaag attttaatga agttttacca gaagggttct tacaacgtac gtccgggaga   1020
```

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06272006\J583110.raw**

```
        550 ggtaaggtaa taggatgggc tccgcagatg gccgtgttgt ctcacaatgc ggtgggagga  1080
        551 ttcgtgtcgc attgcggctg gaactcgacg ttggagagtg tttggtgcgg agtgccaatg  1140
        552 gccgtgtggc cattggcggc cgagcaacat gcgaacgcgt tccagttggt gaaggagttg  1200
        553 ggaattgcgg tggagattaa gatggattat aggaagaaca gtggtgtgat tgtggaggca  1260
        554 aaaatgattg agaaaggaat cagggagttg atggacccgg aaaatgagat aaggggtaat  1320
W-->    555 gtgaaagtga tgaaaaagga gagtaggana gctgtcgtgg atggtgggac ttcttttgat  1380
        556 tacttggatc gttttgttga aactgtcgtg aataatgttt tgtga                   1425
        558 <210> SEQ ID NO: 21
        559 <211> LENGTH: 1446
        560 <212> TYPE: DNA
E-->    561 <213> ORGANISM:  ← response needed
W-->    562 <220> FEATURE:
W-->    563 <221> NAME/KEY:
        564 <222> LOCATION:
        565 <223> OTHER INFORMATION: (pSPB1615)
W-->    566 <400> SEQUENCE: 21
        567 atgggttccg tagccggaaa cagttacaaa cggcctcatg ctgtgtgcat acccttcccg    60
        568 gcgcagggc acatcaaccc catgctgaag ttggccaaac tcctccacca aaagggcttc   120
        569 cacatcacat tcgtcaacac agagtacaac caccgccgct tgctcaagtc cctcggcccc   180
        570 gacgctctcg atggcttgcc ggatttccga ttcgcaacca tccccgacgg tcttcctccg   240
        571 tctgacgcgg acgtcactca ggatgttcct tctctttgta tgtccaccac taacacttgc   300
        572 ttggagccct ttaccgagtt gctgttgaaa ctcaataact ccggcccgga cgtgccaccg   360
        573 gtgacctgca tcgtctcgga tggtgtcatg agcttcacat tgaaggcggc ggagaggttt   420
        574 gcgctgccgg aagtgctgtt ctggacgacg agtgcgtgtg gtttcttggc gtacacgcag   480
        575 tataagcgtc tcttggagaa aggctatgtc cctctcaaag atatgagcca gttaacaaat   540
        576 agctatctgg aaacaaccct cgactgggtt ccaggaatga aggatatccg attaagggac   600
        577 ttcccatcat tcatcaggac aacggatcca aaagacatca tgtacaattt cgtattacaa   660
        578 gaaaccgacg ctgtctccag agccaaagct ctgatcatca acacctttca tacattggaa   720
        579 cacgacgttg taaatgccct ctccaccatg tttccacgtg tttacaccat cggctctctt   780
        580 cagctgatgt tggaccaagt tcatgacaag agccttaacg ccatcaactc caatctctgg   840
        581 aaagaagaat cgcaatgcat cgattggctc aattcaaaag agcccgaatc cgttgtgtat   900
        582 gtgaatttcg gtagtgtcac tgttgtgact gctcaacaac tgacggaatt tgcgtggggg   960
        583 cttgcgaaca gcaacaagac tttttatgg gttattaggc ctgatatagt tgttggagac  1020
        584 tcggcaatgc tgccccctga attcttgacg gacacggaag acagaagcat gctaataagc  1080
        585 tggtgtaacc aagaacaggt gttgaggcac ccttccatcc gaggattttt gacgcacagt  1140
        586 ggttggaact cgacgcttga aagtattgtc agcggagtgc ctatgatatg ttggcctttc  1200
        587 tttgctgagc aacagacaaa ttgtaggttc agttgcgtgg aatgggaaat aggaatggag  1260
        588 attgacaata atgtgaagag agatgaggtt gaggtgctgg tgagagagtt gatggatggt  1320
        589 gaaaaggga agaaatgaa gaagaaagct atggagtgga agatgaaagc agaagcagca  1380
        590 gctgccctg ggggaccttc gtctttaaat ttggaaaaac ttattgagga ggtgcttttg  1440
        591 caataa                                                            1446
        593 <210> SEQ ID NO: 22
        594 <211> LENGTH: 1308
        595 <212> TYPE: DNA
E-->    596 <213> ORGANISM:  ← response needed
W-->    597 <220> FEATURE:
W-->    598 <221> NAME/KEY:
        599 <222> LOCATION:
        600 <223> OTHER INFORMATION: (pSPB660)
```

[handwritten annotations in right margin: "needs exploration (see item 9 on Error Summary Sheet)"]

RAW SEQUENCE LISTING   DATE: 06/27/2006
PATENT APPLICATION: US/10/583,110   TIME: 11:56:31

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272006\J583110.raw

```
W--> 601 <400> SEQUENCE: 22
     602 atgaaggctc atgcagtgat gcttccttgc cccgtacaag ggcacttaaa tcctatgctg     60
     603 aaactggcca aaatattgca ttcaagaggc ttcttcatca cattcgtgaa cacggaattc    120
     604 aatcacaatc gtctagtgcg tgcgagaggc cccgaatctg ttaaaggtcg cgatgatttt    180
     605 cagttcaaaa ccatacctga tggactaccg ccttttgata aggacgcaac gcaagacata    240
     606 cctcaactgt gtgattctct tcaaaagaat ggtcttcctc cattgttgga cctcattaaa    300
     607 agtattaatg attcaccgga ctgtccaaat gttacctgta tagtgattga tttggccatg    360
     608 agtttcgctc ttgatgcggc cgaggtgttc aaaattccca cggtgtactt ttcgccaact    420
     609 agtgcttgtg gattcatggg gttttgcaat tatgaagagc ttgtgaatcg aggattgttt    480
     610 ccacttaaag atgaaagtca ataactaat ggctatcttg ataccaaact agactgggtg    540
     611 ccagggatga agaacattag gctcagagat tttcctagtt tcatccgaac gactgatcca    600
     612 gatgatatca tggtgaactt catgattttt aacatgaaga atgcgcctcg tgcaaaggct    660
     613 gtggtagtca acacattcga tgaattggag aaagatgtat tggaggccct aagtaaaaaa    720
     614 tttgatcatg ttttttccat aggcccactc caattgatgg agaaggcttt ccaaaagcct    780
     615 gaggtaaaat ctataggatc aagcttgtgg aaagaagaca acacgtgcat cgcctggctc    840
     616 aacggcaggg agccaaattc tgtgttgtac gtgaactttg gaagcatcac agtgttgtca    900
     617 cctcaacaac tattggagtt cgcatggggc ctagccaata gcaaccatta ctttttgtgg    960
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     619 gaagttgaag ggcgggcgat gatggtgcgt tggtgctctc aagagcaagt attggcccat   1080
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